



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LaVallie, Edward  
Racie, Lisa
- (ii) TITLE OF INVENTION: HUMAN SDF-5 PROTEIN AND COMPOSITIONS
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: GENETICS INSTITUTE, INC.  
(B) STREET: 87 CAMBRIDGE PARK DRIVE  
(C) CITY: CAMBRIDGE  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02140
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/949,904  
(B) FILING DATE: October 15, 1997  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: LAZAR, STEVEN R.  
(B) REGISTRATION NUMBER: 32,618
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (617) 498-8260  
(B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2027 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCC TTCATGGCCT AGCTCATTCT GCTCCCCCGG GTCGGAGCCC CCCGGAGCTG

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99 FEB -3 AM 8:03  
GROUP 180

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CGCGCGGGCT	TGCAGCGCCT	CGCCCCGCGT	CCTCCCGGTG	TCCCGCTTCT	CCGCGCCCCA	120
GCCGCCGGCT	GCCAGCTTTT	CGGGGCCCCG	AGTCGCACCC	AGCGAAGAGA	GCGGGCCCCG	180
GACAAGCTCG	AACTCCGGCC	GCCTCGCCCT	TCCCCGGCTC	CGCTCCCTCT	GCCCCCTCGG	240
GGTCGCGCGC	CCACGATGCT	GCAGGGCCCT	GGCTCGCTGC	TGCTGCTCTT	CCTCGCCTCG	300
CACTGCTGCC	TGGGCTCGGC	GCGCGGGCTC	TTCTCTTTTG	GCCAGCCCGA	CTTCTCCTAC	360
AAGCGCAGCA	ATTGCAAGCC	CATCCCGGCC	AACCTGCAGC	TGTGCCACGG	CATCGAATAC	420
CAGAACATGC	GGCTGCCCAA	CCTGCTGGGC	CACGAGACCA	TGAAGGAGGT	GCTGGAGCAG	480
GCCGGCGCTT	GGATCCCGCT	GGTCATGAAG	CAGTGCCACC	CGGACACCAA	GAAGTTCCTG	540
TGCTCGCTCT	TCGCCCCCGT	CTGCCTCGAT	GACCTAGACG	AGACCATCCA	GCCATGCCAC	600
TCGCTCTGCG	TGCAGGTGAA	GGACCGCTGC	GCCCCGGTCA	TGTCCGCCTT	CGGCTTCCCC	660
TGGCCCGACA	TGCTTGAGTG	CGACCGTTTC	CCCCAGGACA	ACGACCTTTG	CATCCCCCTC	720
GCTAGCAGCG	ACCACCTCCT	GCCAGCCACC	GAGGAAGCTC	CAAAGGTATG	TGAAGCCTGC	780
AAAAATAAAA	ATGATGATGA	CAACGACATA	ATGGAAACGC	TTTGTA AAAA	TGATTTTGCA	840
CTGAAAATAA	AAGTGAAGGA	GATAACCTAC	ATCAACCGAG	ATACCAAAAT	CATCCTGGAG	900
ACCAAGAGCA	AGACCATTTA	CAAGCTGAAC	GGTGTGTCCG	AAAGGGACCT	GAAGAAATCG	960
GTGCTGTGGC	TCAAAGACAG	CTTGCA GTGC	ACCTGTGAGG	AGATGAACGA	CATCAACGCG	1020
CCCTATCTGG	TCATGGGACA	GAAACAGGGT	GGGGAGCTGG	TGATCACCTC	GGTGAAGCGG	1080
TGGCAGAAGG	GGCAGAGAGA	GTTCAAGCGC	ATCTCCCGCA	GCATCCGCAA	GCTGCAGTGC	1140
TAGTCCCGGC	ATCCTGATGG	CTCCGACAGG	CCTGCTCCAG	AGCACGGCTG	ACCATTTCTG	1200
CTCCGGGATC	TCAGCTCCCG	TTCCCCAAGC	ACACTCCTAG	CTGCTCCAGT	CTCAGCCTGG	1260
GCAGCTTCCC	CCTGCCTTTT	GCACGTTTGC	ATCCCCAGCA	TTTCCTGAGT	TATAAGGCCA	1320
CAGGAGTGGA	TAGCTGTTTT	CACCTAAAGG	AAAAGCCAC	CCGAATCTTG	TAGAAATATT	1380
CAAAC TAATA	AAATCATGAA	TATTTTTATG	AAGTTTAAAA	ATAGCTCACT	TTAAAGCTAG	1440
TTTTGAATAG	GTGCAACTGT	GA CT TGGGTC	TGGTTGGTTG	TTGTTTGTG	TTTTGAGTCA	1500
GCTGATTTTC	ACTTCCCACT	GAGGTGTGCA	TAACATGCAA	ATTGCTTCAA	TTTTCTCTGT	1560
GGCCCAA ACT	TGTGGGTCAC	AAACCCTGTT	GAGATAAAGC	TGGCTGTTAT	CTCAACATCT	1620
TCATCAGCTC	CAGACTGAGA	CTCAGTGTCT	AAGTCTTACA	ACAATTCATC	ATTTTATACC	1680
TTCAATGGGA	ACTTAAACTG	TTACATGTAT	CACATTCCAG	CTACAATACT	TCCATTTATT	1740

AGAAGCACAT TAACCATTTC TATAGCATGA TTTCTTCAAG TAAAAGGCAA AAGATATAAA 1800  
 TTTTATAATT GACTTGAGTA CTTTAAGCCT TGTTTAAAC ATTTCTTACT TAACTTTTGC 1860  
 AAATTAAACC CATTGTAGCT TACCTGTAAT ATACATAGTA GTTTACCTTT AAAAGTTGTA 1920  
 AAAATATTGC TTTAACCAAC ACTGTAAATA TTTCAGATAA ACATTATATT CTTGTATATA 1980  
 AACTTTACAT CCTGTTTTAC CTAAAAA AAAAAG CGGCCGC 2027

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Leu	Gln	Gly	Pro	Gly	Ser	Leu	Leu	Leu	Leu	Phe	Leu	Ala	Ser	His	1	5	10	15
Cys	Cys	Leu	Gly	Ser	Ala	Arg	Gly	Leu	Phe	Leu	Phe	Gly	Gln	Pro	Asp	20	25	30	
Phe	Ser	Tyr	Lys	Arg	Ser	Asn	Cys	Lys	Pro	Ile	Pro	Ala	Asn	Leu	Gln	35	40	45	
Leu	Cys	His	Gly	Ile	Glu	Tyr	Gln	Asn	Met	Arg	Leu	Pro	Asn	Leu	Leu	50	55	60	
Gly	His	Glu	Thr	Met	Lys	Glu	Val	Leu	Glu	Gln	Ala	Gly	Ala	Trp	Ile	65	70	75	80
Pro	Leu	Val	Met	Lys	Gln	Cys	His	Pro	Asp	Thr	Lys	Lys	Phe	Leu	Cys	85	90	95	
Ser	Leu	Phe	Ala	Pro	Val	Cys	Leu	Asp	Asp	Leu	Asp	Glu	Thr	Ile	Gln	100	105	110	
Pro	Cys	His	Ser	Leu	Cys	Val	Gln	Val	Lys	Asp	Arg	Cys	Ala	Pro	Val	115	120	125	
Met	Ser	Ala	Phe	Gly	Phe	Pro	Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	130	135	140	
Phe	Pro	Gln	Asp	Asn	Asp	Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	145	150	155	160
Leu	Leu	Pro	Ala	Thr	Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys				



Pro	Val	Cys	Leu	Asp	Asp	Leu	Asp	Glu	Thr	Ile	Gln	Pro	Cys	His	Ser		
				85					90					95			
Leu	Cys	Val	Gln	Val	Lys	Asp	Arg	Cys	Ala	Pro	Val	Met	Ser	Ala	Phe		
			100					105					110				
Gly	Phe	Pro	Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp		
		115					120					125					
Asn	Asp	Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala		
		130				135					140						
Thr	Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp		
145					150					155					160		
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	Leu		
				165					170					175			
Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	Lys	Ile		
			180					185					190				
Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	Gly	Val	Ser		
		195					200					205					
Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	Asp	Ser	Leu	Gln		
	210					215					220						
Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	Pro	Tyr	Leu	Val	Met		
225					230					235					240		
Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	Thr	Ser	Val	Lys	Arg	Trp		
			245					250						255			
Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	Ile	Ser	Arg	Ser	Ile	Arg	Lys		
			260					265					270				
Leu	Gln	Cys															
		275															

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CATGGGCAGC TCGAG

15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 34 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGCAGGCGA GCCTGAATTC CTCGAGCCAT CATG

34

(2) INFORMATION FOR SEQ ID NO:6:

- C'*  
*Cont*
- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 83 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCCTGTGGG TAGAACGAGG TTAAAAAACG TCTAGGCCCC CCGAACCACG GGGACGTGGT

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TTTCCTTTGA AAAACACGAT TGC

83